

BLASTX ALIGNMENT OF SEQ ID NO: 4, CADHERIN-LIKE POLYPEPTIDE WITH HUMAN OB-CADHERIN-1 POLYPEPTIDE SEQ ID NO: 16

Query: Cadherin-like pypeptide (SEQ ID NO: 4)
 Subjct: dbj|BAA04798.1| (D21254) OB-cadherin-1 [Homo sapiens] (SEQ ID NO: 16)
 Length = 796

Score = 1478 (525.3 bits), Expect = 2.1e-164, Sum P(2) = 2.1e-164
 Identities = 269/419 (64%), Positives = 341/419 (81%), Frame = +1

Query: 283 GPALLRTRRSWVNQFFVIEEYAGPEPVLIGKLHSDVDRGGRTKYLLTGEGAGTVFVID 462
 G L R++R WVNQFFVIEEY GP+PVL+G+LHSD+D G+G KY+L+GEGAGT+FVID
 Sbjct: 45 GQVLQRSKRGWVNQFFVIEEYTGDPVLVGRHLSDSDGDNKIKYILSGEGAGTIEVID 104

Query: 463 EATGNIHVTKSLDREERAKQYVLLAQAVDRASNRPLEPSEFIIKQDINDNPPIFPLGPY 642
 + +GNIH TK+LDREE+AQY L+AQAVDR +NRLEPSEFI+K QDINDNPP F Y
 Sbjct: 105 DKSGNIHATKTLDREERAQYTLMAQAVDRDNRPLEPSEFIVKQDINDNPPFEFLHETY 164

Query: 643 HATVPEMSNVGTSVIQVTAHDADDPYNSAKLVYTVLDGLPFFSVDPQTGVVRTAIPNM 822
 HA VPE SNVGTSVIQTADDDP+YGNLSAKLVY++L+G P+FSV+ QTG++RTA+PNM
 Sbjct: 165 HANVPERSNVGTSVIQVTAHDADDPYNSAKLVYSILEGQPYFSVEAQTGIIRTAIPNM 224

Query: 823 DRETQEEFLVVIQAKDMGGMGLSGSTTVTTLSDVNDNPPKFPQSLYQFSVVEAGPG 1002
 DRE +EE+ VVIQAKDMGGMGLSG+T VT+TL+DVNDNPPKFPQS+YQ SV E A PG
 Sbjct: 225 DREAKEYHVVIQAKDMGGMGLSGTKVTITLTDVNDNPPKFPQSVYQISVSEAAVPG 284

Query: 1003 TLVGRRLAQDQDPLGDNALMAYSILDGSEAFSISTDLQGRDGLLTVRKPLDFESORSYS 1182
 VGR++A+DPD+G+N L+ Y+I+DG+G E+F I+TD + ++G++ ++KP+DFE++R+YS
 Sbjct: 285 EEVGRVKAKDPDIGNGLVTVYNIVDGDMESFEITTDYETQEGVIKPKPVDFTKRAYS 344

Query: 1183 FRVEATNTLIDPAYLRRGPFKDVASVRVAVQDAPEPPAFTQAAHYHLTVPENKAPGTLVGQ 1362
 +VEA N IDP ++ GPFKD +V++AV+DA EPP F +Y V EN A GT+VG+
 Sbjct: 345 LKVEAANVHIDPKFISNGPFKDTVTVKIAVEDADEPPMFLAPSYIHEVQENAAAGTVVGR 404

Query: 1363 ISAADLDSPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARAWNHLTVLATEL 1539
 + A D D+ SPIRYSI H+D +R +I PE+G I T PLDRE AW N+TV A E+
 Sbjct: 405 VHAKDPDAANSPIRYSIDRHTDLDRFFTNPEDGFIKTKPLDREETAWLNITVFAAEI 463

FIG. 1

**BLASTX ALIGNMENT OF SEQ ID NO: 4, CADHERIN-LIKE POLYPEPTIDE WITH HUMAN
SEQUENCE ENCODED BY HUMAN OSF-4-1 cDNA POLYPEPTIDE SEQ ID NO: 17**

Query: Cadherin-like plypeptide (SEQ ID NO: 4)
 Subjct: sp|R49731|R49731 Sequence encoded by human OSF-4-1 Cdna (SEQ ID NO: 17)
 Length = 796

Score = 1478 (525.3 bits), Expect = 1.2e-164, Sum P(2) = 1.2e-164
 Identities = 269/419 (64%), Positives = 341/419 (81%), Frame = +1

Query: 283 GPALLRRSWVNQFFVIEEYAGPEPVLIGKLHSDVDRGEGRTKYLTTGEGAGTVFVID 462
 G L R++R WVNQFFVIEEY GP+PVL+G+LHSD+D G+G KY+L+GEGAGT+FVID
 Sbjct: 45 GQVLQSKRGWVNQFFVIEEYTGPDPLVGLRLHSDIDSDGDNIKYILSGEGAGTIFVID 104

Query: 463 EATGNIHVTKSLDREERKQYVLLAQAVDRASNRPLEPSEFIIKQDINDNPPIFPLGPY 642
 + +GNIH TK+LDREE+AQY L+AQAVDR +NRLEPSEFI+K QDINDNPP F Y
 Sbjct: 105 DKSGNIHATKTLTREERAQYTLMAQAVDRDTRNRPSEFIVKVQDINDNPPEFLHETY 164

Query: 643 HATVPEMSNVGTSVIOVTAHDADDPSYNSAKLVYTVLDGLPFEVSVDPTGVVRTAIPNM 822
 HA VPE SNVGTSVIOVTA DADDP+YGNsAKLVY++L+G P+FSV+ QTG++RTA+PNM
 Sbjct: 165 HANVPERSNVGTSVIOVTAHDADDPTYGNSAKLVYSILEGQPYFSVEAQTGIIRTAIPNM 224

Query: 823 DRETQEEFLVVIQAKDMGGMGLSGSTVTVTLSVDNDNPPKFPQSLYQFSVVETAGPG 1002
 DRE +EE+ VVIQAKDMGGMGLSG+T VT+TL+DVNDNPPKFPQS+YQ SV E A PG
 Sbjct: 225 DREAKEYHVVIQAKDMGGMGLSGTKVTITLTDVNDNPPKFPQSVYQISVSEAAVPG 284

Query: 1003 TLVGRILRAQDPDLGDNALMAYSILDGEGSEAFSISTDLQGRDGLLTVRKPLDFESQRSYS 1182
 VGR++A+DPD+G+N L+ Y+I+DG+G E+F I+TD + ++G++ ++KP+DFE++R+YS
 Sbjct: 285 EEVGRVKAKDPDIDGGLVTVNIIVDGMESFEITTDYETQEGVIKPKPVDFTKRAYS 344

Query: 1183 FRVEATNTLIDPAYLRGPFKDVASVRVAVQDAPEPAFTQAAHYHLTVPENKAPGTLVGQ 1362
 +VEA N IDP ++ GPFKD +V++AV+DA EPP F +Y V EN A GT+VG+
 Sbjct: 345 LKVEANVHIDPKFISNGPFKDTVTVKIAVEDADEPPMFLAPSYIHEVQENAAAGTVVGR 404

Query: 1363 ISAADLDSPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARAWNLTVLATEL 1539
 + A D+ SPIRYSI H+D +R F+I PE+G I T PLDRE AW N+TV A E+
 Sbjct: 405 VHAKDPAANSPIRYSIDRHTDLDRFTINPEDGFIKTKPLDREETAWLNITVFAAEI 463

FIG. 2